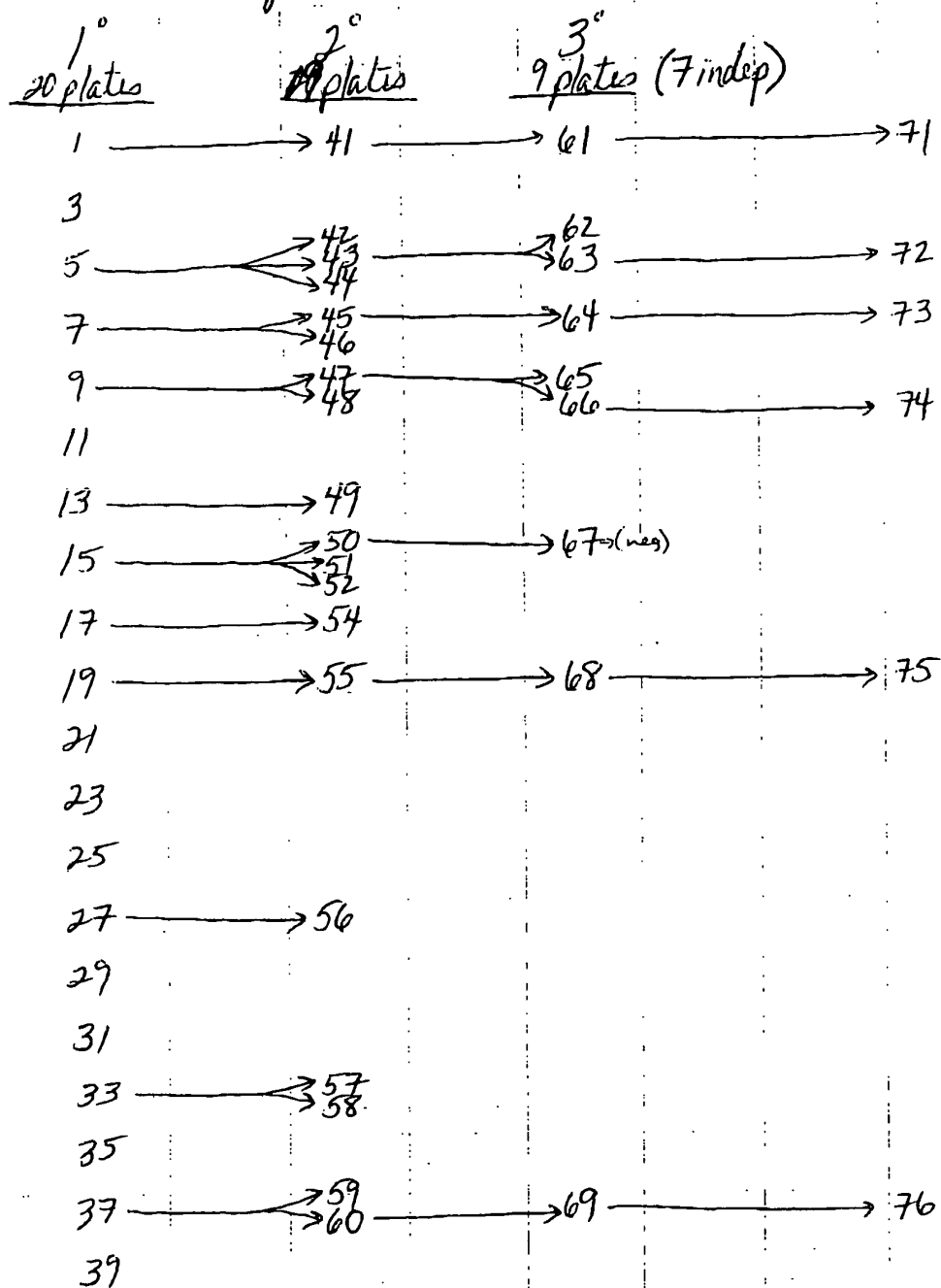


Exhibit 9

Lab Notebook Pages of
Dr. Susan L. Acton

Successive Rounds of screening to clone the murine SR-BI from a 3T3-L1 Adipocyte cDNA Library



Probe: 500-600 bp BamHI fragment (5') of hSR-BI in pcDNA1

3T3-L1 Adipocyte Library

pcDNA1 in MC1061/P3

G. Balclini electroporated & plated bugs, then scraped plates & froze. This is what she gave me. (3 vials)

Use vial 2

Scrape a little & thaw, dilute 1:100, then 1:50 and plate 300 μ l on a 10 cm plate

She did 20 plates of 30,000 colonies (must have been very small 'colonies')

Note that the library is non-directional & is in the ~~Bst~~XI sites in pcDNA1

X158 Screen 3T3-L1 Adipocyte Library for murine SR-BI

Purpose: Clone the murine SR-BI for further analysis

Plate Library

Pour 100mm LB Amp/Tet (15/8 μ g/ml) Plates
let dry 48 hrs r.t.

Scrape some bugs from frozen tube 2 (from
G. Baldwin, Lodish lab) of 3T3-L1 library in
MC1061/P3 pCDNA1 expression
thaw scraped bugs, dilute 1:100, then 1:17
and plate 50 μ l

2 ml undil bugs tube #2
198 μ l LB

200 μ l of 1:100
 \hookrightarrow 118 μ l of 1:100
1.88 μ l of LB

2 ml of 1:17
 \hookrightarrow plate 50 μ l/100mm plate

Incubate plates 14 hrs (6pm-8pm) 37°C
Transfer plates to 4°C /hr

Make lifts

- ① Carefully lay down sterile Nitrocellulose
Millipore/HATF prenumbered, number side down
onto bugs
- ② When wet, poke 3 holes thru membrane and
plate
- ③ Lift filter off plate with blunt end forceps

- ~~Loop~~
- ④ Lay bug side up onto fresh LB A/T plate
 - ⑤ Lay another filter (pre-numbered) numby-side down onto bugs on filter to make sandwich
 - ⑥ Poke holes thru duplicate filter to match holes in original filter
 - ⑦ Let bugs grow 3 hrs 37°C between filters
 - ⑧ Let bugs regrow on original filter plate 3 hrs. Then store wrapped in parafilm 4°C.
 - ⑨ As in Maniatis, (1.98) lyse colonies
Set up 4 trays with whatman 3MM Paper soaked with (in order)
 - ① 10% SDS
 - ② Denaturing soln. (0.5M NaOH, 1.5M NaCl)
 - ③ Neutralising soln (1.5M NaCl, 0.5M Tris-Cl pH 7.4)
 - ④ 2X SSC
 - a) Peel nitrocellulose sandwich from gel & place on SDS-impregnated 3MM paper 8-3 min
 - b) Wipe off excess with edge of tray & transfer to denat. tray 5 min
 - c) Transfer to Neutral tray 5 min
 - d) Transfer to 2X SSC tray ~~5 min~~ but separate sandwiches first - 5 min
 - e) Transfer to dry 3MM paper colony side up
Dry at least 30 min r.t.
 - ⑩ Sandwich filters between 2 sheets of dry 3MM paper. Fix by baking 1 hr 80°C in vacuum oven
 - ⑪ Store filters under vacuum no heat

X158 cont'dMake SR-BI probe

Digest #		10X Ac BSA	H ₂ O	10X NEB Buffer	enzyme
① phasRIII (1.03 µg/µl)	10 µl	5 µl	28 µl	5 µl #2	PSI/HindIII 1 µl/1 µl
② pcDNA1 (1 µg/µl)	10 µl	5 µl	28 µl	5 µl #2	↓
③ phasRIII	10 µl	5 µl	28 µl	5 µl	BamHI ↓
④ pcDNA1	10 µl	5 µl	28 µl	5 µl	buffer ↓

Incubate 37°C 2hr 2:10-4:10 freeze digest
 Ran mini-gel; all digests looked good.
 Clean up digests ① + ③

Phenol extract (50 µl)
 Back extract w/ 50 µl TE
 Precip DNA in 100 µl
 with 10 µl 3M NaOAc
 260 µl 100% EtOH
 -80°C 20 min
 Spin 20 min 4°C
 Wash w/ 70% EtOH (cold)
 Speed vac Dry
 Resuspend in 15 µl TE
 Add 5 µl 10X blue juice
 Heat 68°C 10 min

Run on 1% Low melt (Seaplaque) TAE gel

λ HindIII 0.174
 AaeIII

Digest ①
 4 lanes

Digest ③
 4 lanes

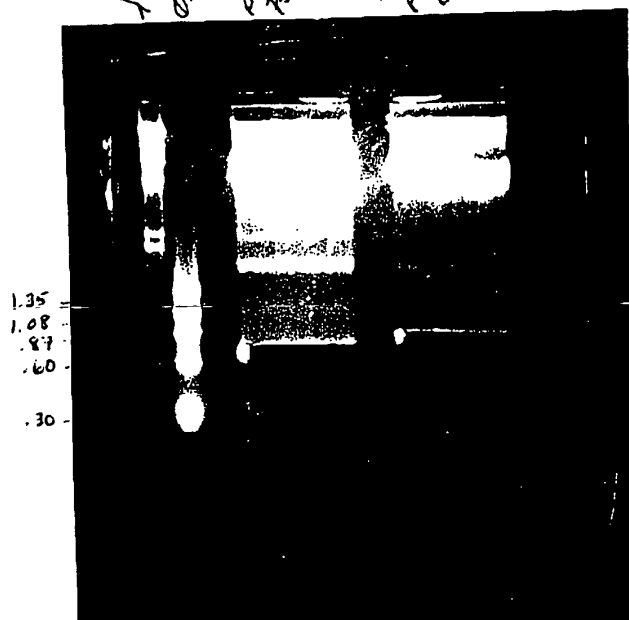
4°C overnight
 6 V
 turned up to
 20 V at noon
 Cut out bands
 at 6 pm

IX58 cont'd

1 Hind III
0X174 Hae III

phase BI
Pst I/Hind III

phase BI
Bam HI



Probes

C. ————— A
 B

D. —————

For screening lifts, use probe B

Label Probe

- ① Melt probe B, take 10ul & add to 10ul H₂O. Label as probe B diluted 1:1
 - ② Combine 5ul diluted probe B
5ul ³²P dCTP (from Amersham kit 9mers)
boil 5'
spin down liquid
 - ③ Add 10ul labeling buffer (kit)
23ul H₂O
2ul enzyme
5ul ³²P dCTP
Mix by pipetting gently
Spin
Put in 37°C warm room ~45 min
2hr
- 2pm - 4pm

[X158] cont'd

Check incorporation

Combine
20 μ l salmon sperm DNA
1 μ l label rxn
180 μ l 5% cold TCA

Spin 10' 4°C
Remove 100 μ l & count as top
Count remainder as bottom

$$\% \text{ incorp} = \frac{\text{bottom} - \text{top}}{\text{bottom} + \text{top}} \times 100\% = 22\%$$

$$\% \text{ incorp} = 22\%$$

Clean up probe:

Add 5 μ l LPA to rxn
25 μ l 7.5 M NH₄ Acetate
125 μ l 100% EtOH (cold)

Put at -80°C 20 min
Spin 20 min 4°C
Rinse w/ cold 70% EtOH
Speed-Vac dry
Resuspend in 30 μ l TE

Add to prehyb sol'n containing filters
Hybridize 50°C overnight

X158 cont'd

Prehyb - 50°C

500 mM PB, 1 mM EDTA, 7% SDS, 1% BSA, 100 µg/ml
salmon sperm DNA (boiled prior to adding)

For 60 mls: 30 mls 1M PB ✓
120 µl 500 mM EDTA ✓
21 mls 20% SDS ✓
0.6g BSA ✓
0.6 ml salmon sperm DNA ✓
8.28 ml H₂O ✓

Hyb - 50°C in prehyb sol'n + probe

Washes -

Wash blot 2X fast w/ 300 mM PB r.t.
wash " 1X 10' " " r.t.
Wash " 2X 10' Sol'n A (300 mM) 54°C
Wash " " " " B (300 mM) 54°C

Put down on film - 48 hrs r.t.

- Let filters air dry on whatman
- Arrange on old piece film covered with saran wrap
- ~~Cover~~ Tape down filters & cover w/ saran wrap
- Put marks (from Stratagene ruler) down to orient film w/ filters

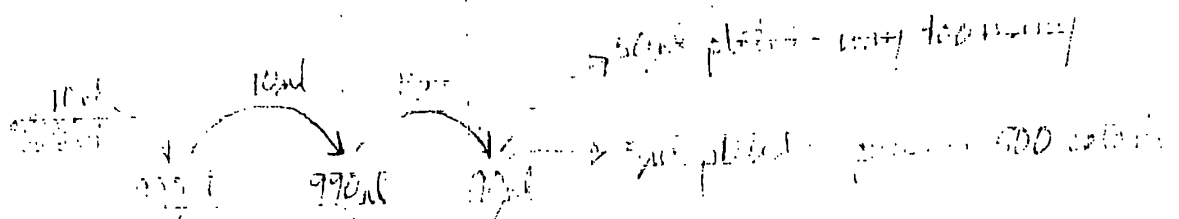
Results:

> 100 small dots which are on duplicate lifts.
Background is low. Looks good!

[X158] cont'd

Secondary Lifts

- A. Picked 19 positive dots,
1 negative control
from primary lifts
- B. Used pasture p/pets, large end to pick
plugs from plates into 0.5 ml LB + Amp/Tet
overnight 37°C
- C. Make dilutions



- D. Plate bugs
First time plated way too many so replated
~13 hrs 37°C
- E. Transfer plates to cold room 1 hr 4°C

Lifts

- ① Carefully lay down sterile HATF nitrocellulose
millipore prenumbered, number side down
onto bugs
- ② When wet, poke 3 holes thru membrane
and plate
- ③ Lift filter off plate with blunt end forceps
- ④ Lay bug side up onto fresh LB A/T plate
(LB can for 54-60)
- ⑤ Lay another filter (labeled B) number
side down onto bugs on filter to make
a sandwich
- ⑥ Poke holes thru duplicate filter to match
holes in original filter

- ⑦ let bugs grow 3 hrs 37°C between filters
 ⑧ let bugs grow on original plate 3 hrs then store wrapped in parafilm 4°C
 ⑨ As in Maniatis (1.98) lyse colonies
 Set up 4 trays with Whatman 3MM paper soaked with

3 min
 5 min
 5 min
 5 min

- ① 10% SDS
 ② Denaturing soln (0.5N NaOH, 1.5M NaCl)
 ③ Neutralizing soln (1.5M NaCl, 0.5M Tris-Cl, pH 7.4)
 ④ 2X SSC

- a) Peel nitro. sandwich from gel & place on SDS-immug. 3MM paper
 b) Wipe off excess with edge of tray & transfer to denat. tray. 5 min
 c) Transfer to neutral tray. 5 min
 d) Transfer to 2X SSC tray after separating filters
 e) Transfer to dry 3MM paper colony side up. Dry at least 30 min r.t.

- ⑩ Sandwich filters between sheets of dry 3MM paper. Fix by baking 1 hr 80°C in vacuum oven
 ⑪ Store filters under vacuum no heat

Label probe (5' BamHI fragment of hSR-BI) as for 1% HTS

USER: JID:DERENKOV PRESET TIME: 1.00 TUI 4.0
 SAMPLE REPEAT: 1 CYCLE REPEAT: 1 SOLIN R523214
 IN: 1.000000 REP: 1
 CHANNEL 1-LL1000 UL1000 ISIGMA: 2.00 BKG STD: 0.00 BKG 2518: 0.00 LOR:
 CHANNEL 2-LL1600 UL1000 ISIGMA: 2.00 BKG STD: 0.00 BKG 7516: 0.00 LOR:
 DATA CALD: CFH, UNKNOWN REPLICATES: 1 NORM FACTOR: 01.00000
 HALF LIFE (DAYS) IN

SAN	CFH1	CFH2	TIME
1	1032136.54	757.00	1.00
2	1037860.97	324.00	1.00

36% incorporation

Do L...L in 11.1 in 1.000 - ~~Not used~~ 6 ok

Wash blots - Note: May have accidentally used 600mM PB
final rather than 300mM

- ① Wash blot 1X fast w/ 300mM PB r.t.
- ② Wash blot 1X 10' r.t. 300mM PB
- ③ Wash 2X 54°C sol'n A 300mM 10' each

Wash A: 300mM PB, 5% SDS, 0.5% BSA, 1mM EDTA

For 500ml: 300ml 0.5M PB
25g SDS
2.5g BSA
1ml 500mM EDTA
H₂O to 500ml

- ④ Wash 2X 54°C sol'n B (300mM PB) 10' each

Wash B: 300mM PB, 1% SDS, 1mM EDTA

300ml 0.5M PB
15ml 20% SDS
1ml 500mM EDTA
H₂O to 500ml

Dry & expose to film

- ① Let filters dry on whatman paper
- ② Use old piece of film as support
wrap it in saran wrap
put filters on it & tape down
put stragene ruler pieces on it to
line up films w/ filters
- ③ Cover with saran wrap
Expose to film 2 days

Results: 2° lifts don't look as good as 1° - should
not have amplified plug pick from 1°. I
think high background may be due
to accidental use of 600mM PB rather
than 300mM PB.

Still there seem to be some definite
positives so picked them for 3°.

Wash 3° as before - 54°C, 300mM
Put down on film - w/screen

X160

Plasmid midiprep

preps: 6 single isolates from 3° screen #71-76

Day 1

1. Pick a single colony into 25 mls LB Amp/Tet and grow overnight shaking 37°C.

Day 2

2. Take 400 μ l out into freezer vial, add 100 μ l glycerol and freeze at -150°C.
3. Transfer remainder to Falcon 2059 15 ml tube on ice.
4. Spin rest in SS-34, 9000 rpm, 2 min 4°C. Add remaining half.
5. Dry pellet as much as possible.
6. Resuspend pellet in 500 μ l ice cold solution I by vigorous vortexing.
7. Add 1 ml fresh solution II (0.2 N NaOH, 1% SDS)
for 100 ml: 1 ml 2 N NaOH
0.5 ml 20% SDS
8.5 mls ddH₂O
Swirl gently until clear. Do not vortex. Leave on ice 10 min.
8. Add 750 μ l solution III (ice-cold). Close tube and mix contents by shaking vigorously several times. Store on ice 5'. A flocculent white precipitate should form.
9. Centrifuge 15', 4°C, 9000 rpm.
10. Recover supe and add equal volume of phenol:chloroform. Mix by vortexing.
11. Spin 9000 rpm, 5'.
12. Add 2 volumes, ethanol r.t., vortex, let stand 5'. Spin in SS-34 rotor for 15' 9,000 rpm.
13. Carefully aspirate off all liquid (want it dry) and rinse once in cold 70% EtOH. Aspirate again getting any extraneous drops. Airdry 10' minutes.
14. Redissolve in 100 μ l TE plus DNase-free RNase (20 μ g/ml). Vortex briefly. Incubate 37°C, 0.5 - 2 hr. Transfer to sterile eppendorf. Refrig 4°C o.n.
15. Quantitate by dilutions onto EtBr plate.
Add DNase-free RNase to final 10 μ g/ml

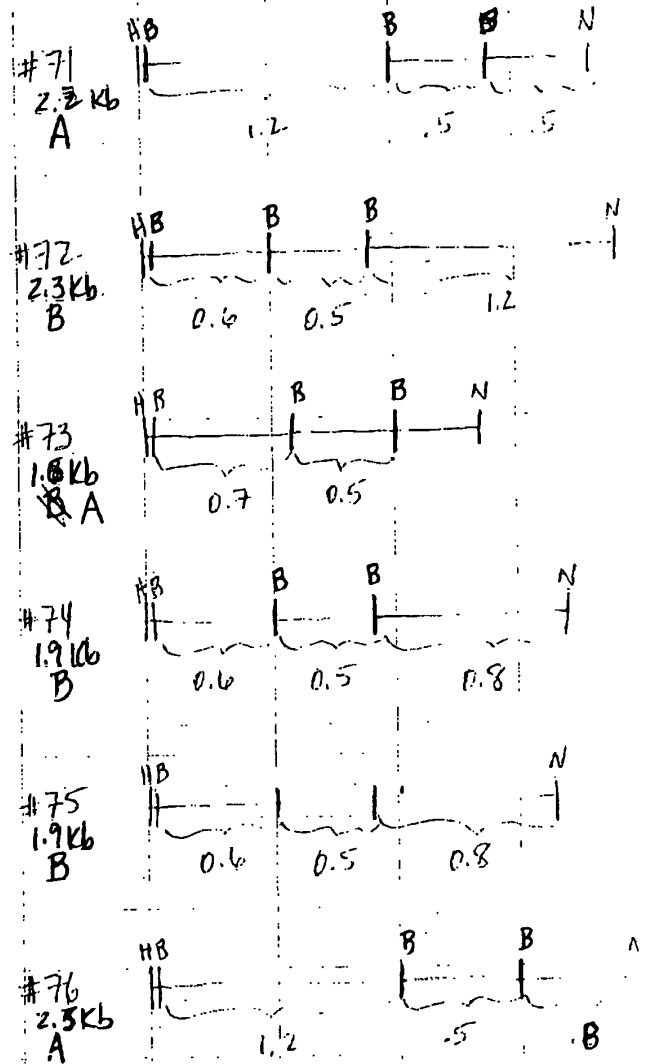
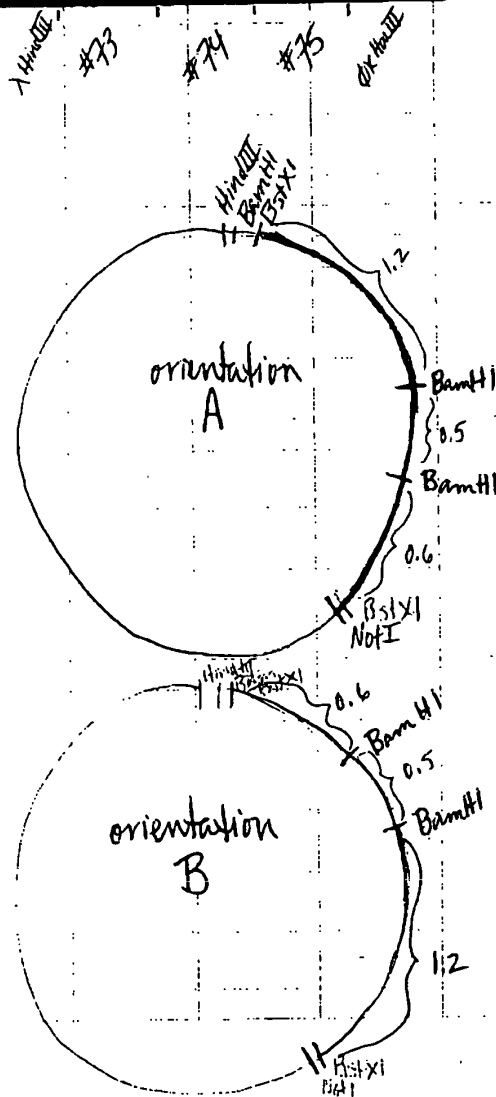
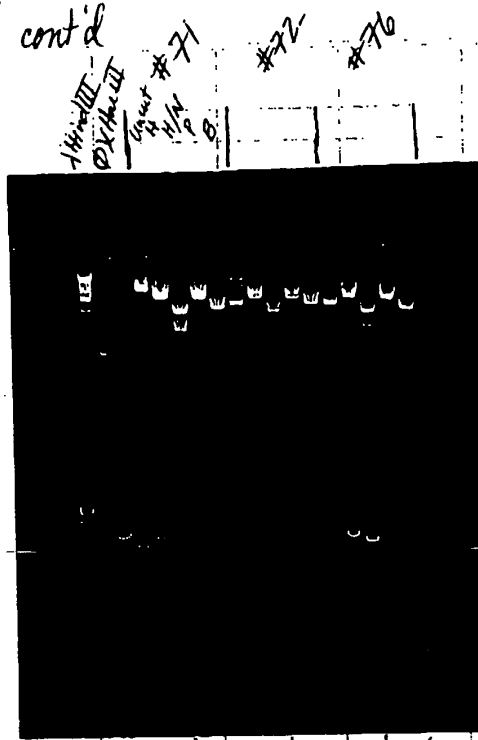
X160
cont'd

Digests of Midi-preps

Digest #	DNA	10X ACPSA ul	NEB Buffer 10X	H ₂ O	Int each enzymes	DNA Prep
1	#71 - 2ul	2ul	2.2ul	14ul	Hind III	O.B.
2			2	13	Hind III / Not I	
3			2	12	Pst I	
4			2	13	Bam HI	
5			u	13		
6	#72					
7						
8						
9						
10						
11	#73					
12						
13						
14						
15						
16	#74					
17						
18						
19						
20						
21	#75					
22						
23						
24						
25						
26	#76					
27						
28						
29						
30						

37°C 11:45am - 2:45

X160 cont'd



Note that orientation B was found to be correct after sequencing of #74 + #76

X161

DEAE dextran transfections of COS M6 cells

materials:

1. 35 mm dishes
2. DMEM with 10% FBS
3. Chloroquine (40 mM in CMF PBS, sterile filtered)
4. DNA
5. CMF PBS
6. DEAE-dextran (10 mg/ml in CMF PBS (autoclaved))
7. DMSO
8. cPBS
9. sterile tips

method:

day 0 (set up cells)

Set COS M6 cells in 100 mm dishes

(Set 1 confluent T75 into 2.25 100 mm dishes; or 1.5×10^6 cells/dish in 10 ml DMEM with 10% FBS)

day 1 (transfect)

1. In sterile polypropylene tubes prepare for each dish add (in order):
 - a) add CMF PBS to 1.9 ml
 - b) DNA - $8 \mu\text{g}$ /dish
 - c) 100 μl of 10 mg/ml DEAE-dextran, vortex well (7 seconds)

tube #	plates	DNA	CMF PBS	10 mg/ml DEAE-dextran
1	1	phsR BI Cl. 1.03 mg/ml 9.7 μl	1.9 ml	100 μl
2	1	#74 (7/22/94) 1.94 mg/ml 5.2 ml	1.9 ml	100 μl
3	1	#76 (7/22/94) 0.85 mg/ml 11.8 μl	1.9 ml	100 μl
4				

2. Rinse cells with 10 mls CMF PBS (37C). Aspirate PBS.
3. Add transfection cocktail from step 1 and distribute evenly. Incubate 30 minutes, distributing liquid every 10 min.
4. Add 8 ml DMEM 10% FBS + 80 μM chloroquine and incubate 37C 2.5 hrs.
5. Aspirate off medium and replace with 5 ml 10% DMSO in DMEM 10% FBS for 2.5 min.
6. Aspirate off and wash once with 10 mls cPBS.
7. Refeed with 10 ml warm DMEM 10% FBS/dish. Incubate overnight.

X/lel cont'd

Lipoprotein 4°C Binding Assay

materials:

1. 6-well dishes
2. DMEM with 10% FBS
3. iodinated and unlabeled lipoprotein
4. Tris-HCl wash buffer
5. Tris-HCl BSA wash buffer
6. 0.1 N NaOH
7. 10 x 75 tubes

method:

day 0: Set up cells

Set transfected COS in 6-well dishes at 1×10^6 cells/well in 3 ml/well DMEM + 10% FBS + 1 mM Nabutyrate.

day 1: Binding assay

1. Cool cells down on ice for 30 minutes.
2. Refeed cells labeled ligand 1 ml/well (Hams + HEPES + 10% FBS).
 2 Hot - ^{125}I -lipoprotein: 10.4 $\mu\text{g}/\text{ml}$ ^{125}I -ALDL (#60 104 $\mu\text{g}/\text{ml}$) LDL #161 B (39 $\mu\text{g}/\text{ml}$)
 1 Hot + cold: + 46.4 $\mu\text{g}/\text{ml}$ M-BSA #230 DR (3.2 $\mu\text{g}/\text{ml}$)
 Incubate 2 hrs 4°C (in cold room) on shaker.
3. Wash cells (1 ml each)
 3X fast with BSA wash buffer
 2X 5 min with BSA wash buffer
 2X fast with Tris wash buffer
4. Add 1.0 ml 0.1 N NaOH. Leave 20 min r.t. on shaker
5. Remove 50 μl to 10 x 75 tube and freeze for Lowry.
6. Count 500 μl of rest of sample.
7. Count 10 μl of medium + label for specific activity.

#74

-	+ LDL	+ M-BSA
1	3	5
2	4	

#76

6	8	10
7	9	

InsR-BI

11	12	13
		14

For 14.5 ml med: 14.5 ml Hams + HEPES + 5% ALCLPDS
 + 145 μl ^{125}I -ALDL (#61)

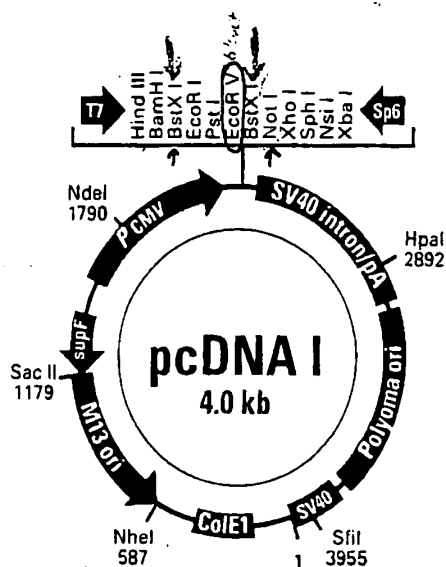
5 ml
 + 51.3 μl LDL #161 B

3 ml
 + 375 μl M-BSA #230

X163 Prepare blunt-cut pcDNA1 for reversing orientation of clone #76 mSR-BI

Purpose: Reverse orientation of clone #76 which appears to be full-length mSR-BI

Approach: Cut mSR-BI out of clone #76 with Hind III/Not I ~~open~~ chew ends to blunt it, ligate into blunt & CIPed pcDNA1



Cut pcDNA1 with EcoRV which is a blunt cutter

DNA	H ₂ O	10X ACBSA	10X NEB Buff 2	EcoRV 20,000 u/ml
#22 (10.5 μg) 15.5 μl (= 20 μg) 10/29/92	14.5 μl	4 μl	4 μl	2 μl
pcDNA1 (1.29 μg/μl)				

Incubate 37°C

12:50 pm - 12:50 pm (Thurs)



← after 3 hrs

Add 60 μl dd H₂O, extract w/ 100 μl phenol:chloroform:isoamylalcohol 25:24:1
Add 10 μl 3M NaOH pH=5, add 250 μl 100% EtOH, Freeze -20°C 1 hr
Spin 10 min 4°C

IX163 cont'd

4 blunt-cut pc-DNA (cont'd) - CIP

redissolve in 90 μ l 10 mM Tris-Cl (pH 8)
remove 2 μ l & save as unCIPed

To remainder add 10 μ l 10X CIP dephosph. buffer
and 8 Units of CIP:

for blunt 1 μ l / 2 pmol, estimate 20 μ g = 16 pmol
so 8 Units CIP

Incubate 15 min at 37°C 3:35 - 3:50

Then ~~add 8 Units more~~ & incubate 45 min at 55°C.
3:50 - 4:35

Kill the CIP

Add 5 μ l 10% SDS & EDTA (pH 8.0) to final 0.5% & 5 mM, respect.
Mix well.
Add proteinase K to final 100 μ g/ml. (10 μ l of 10 mg/ml)
Incubate 30 min 56°C. (4:50 - 5:20 pm)

Cool the rxn to r.t.

Extract once w/ phenol once w/ phenol:chloroform

Add 1/10 vol 3M NaOAc pH 5.0 (10 μ l)

Mix well add 25% EtOH (250 μ l)

Mix & store @ -20°C 2 1/2 hrs

Centrifuge

wash pellet w/ 70% EtOH

Redissolve in TE

Ran overnight on 1% Nusieve (should have been Seaplaque)
Agarose gel. Band was wavy, but cut it out anyway

X164 Prepare #76 mSR-BI cDNA for reinserting into pCDNA1 in correct orientation

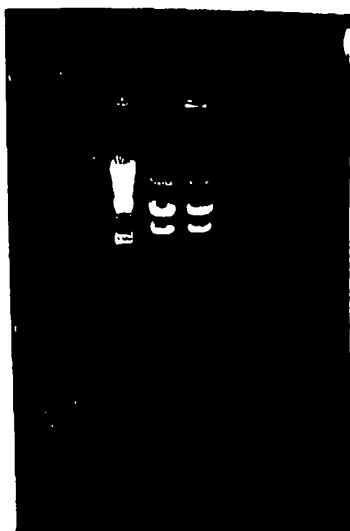
Purpose: Cut out #76 insert to be reinserted in sense orientation. #76 plasmid appears to be full-length mSR-BI but is in the incorrect orientation in pCDNA1.

Digest #76 plasmid:

	DNA	H ₂ O	10X AcBSA	10X NotI buffer	HindIII	NotI
①	#76 (0.85 µg/µl) 24 µl (= 20 µg)	4 µl	10	10 (NotI)	5	5
②	#76 24 µl	4 µl	10	10 µl (NEB L)	5	5

5:45 pm 8:15 pm 37°C

Remove 2 µl from each and analyze on 1% SeaKem GT6 Agarose TAE gel



To the remainder add 10 µl 3M NaAc & 250 µl 100% EtOH
Store at -20°C for 15 min
Spin 10 min 4°C
Wash w/ 70% EtOH
Resuspend in TE (30 µl)
Add 4 µl 10X blue juice

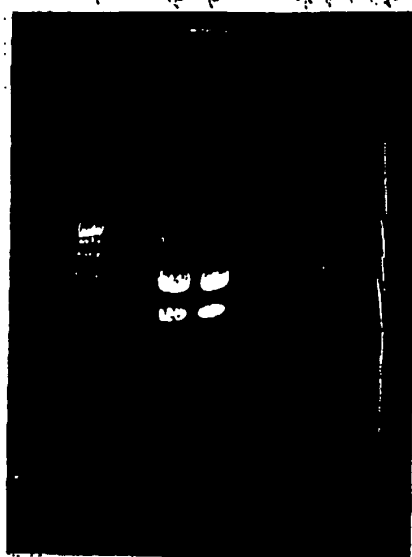
To blunt ends, add 5 μ l 10X T4 DNA Polymerase Buffer
 + 2 μ l of dNTP mix (25mM) for final 1mM
 + 7 μ l H₂O = 50 μ l rxn ~~37° 30 min~~
 + 1 μ l T4 DNA Polymerase 3U/ μ l 37° 30 min (11:30am-12 noon)

Add 4 μ l 0.25M EDTA
 Add 55 μ l Phenol/Chloroform/Isoamyl Alcohol (25:24:1)
 Shake, spin, save aq. layer

To aq. phase
 Add 10

1/10 V 5M NaCl (= 5 μ l)
 Shake add 5 μ l of 1X (near polyacryl)
 add 150 μ l 100% EtOH
 Chill @ -80°C 10'
 Spin 10' 4°C
 Wash pellet w/ 70% EtOH
 Speed vac dry

Resuspend pellet in 36 μ l TE
 Run 3 μ l on mini-gel



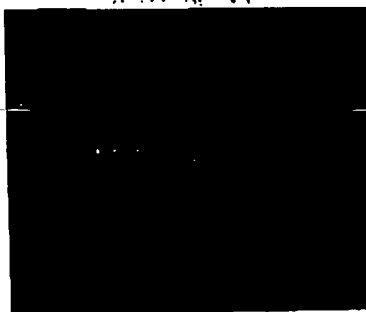
Add blue juice & run on 1% TAE SeaPlaque agarose gel
 in cold room at 20 V (med size app)
 5:45pm - 11:00am
 Cut out insert (~2.3KB) & ligate into vector (see following page.)

1X16.5

Ligation Exns.

- 1) Run blunt vector + blunt insert on 1% GTC Seakem gel to quantitate relative amounts

vector
DNA insert



Estimate that 3 μ l vector = 3 μ l cDNA

Want ~ twice as much insert as vector
in 10 μ l rxn so use
4 μ l vector and 6 μ l insert

- 2) Heat tubes to 70°C for 10-15 min to melt agarose.
3) Combine aliquots of melted gel slices in tubes prewarmed to 70°C.

tube	vector		blunt cDNA insert	H ₂ O	ligase	2X ligation rxn mix (10-100)
	CTP	not CTP				
1	4 μ l	-	-	6 μ l	✓	10 μ l
2	4 μ l	-	6 μ l	4 μ l	✓	↓
3	4 μ l	-	6 μ l	4 μ l	✓	↓
4	-	4 μ l	-	6 μ l	✓	↓

2X Lig rxn mix:

10 μ l	1M Tris-Cl	pH 7.5
1 μ l	1M MgCl ₂	
1 μ l	1M DTT	
1.2 μ l	80 mM ATP	
86.3 μ l	H ₂ O	
100 μ l		

Take 38 μ l & add 4 μ l T4 DNA Ligase

Incubate 48 hr 12-16°C (2 pm Sat - 17 pm Mon)

X/65 cont'd

Transformation of Ligations into MC1061/P3 E. coli

1. Melt the agarose ligation mixtures at 70°C for 10-15 min.
2. Meanwhile thaw competent MC1061/P3 (from J. Ashkenazi)

transform				Results # colonies
1	Lig #1	CIPed vector	5µl	56
2	Lig #2	insert (cDNA) only	5µl	2.8
3	Lig #3	CIPed vector + insert	5µl	30
4	Lig #4	uncIPed vector	5µl	>500
5	TE only		5µl	47
6	pCDNA1 - 100ng/µl		1µl	>500

3. Add 5µl of melted agarose ligation mixtures or control aliquots.
Mix by gentle shaking
Store on ice 30 min 12:45-1:15
4. Transfer to circulating water bath at 42°C
Incubate exactly 90 sec. DO NOT SHAKE TUBES.
5. Rapidly transfer to ice bath. Allow cells to chill 1-2 min.
6. Add 400µl LB medium warm to 37°C & transfer to shaking incubator at 37°C. Incubate 1 hr
1:25-2:25
7. Plate onto LB Amp/Tet (15µg/µl/8µg/µl) plates
100µl/100mm plate
Incubate 37°C overnight

Results: Insert did not ligate into CIPed vector. Vector is CIPed well. Try ~~the~~ blunting cDNA again and GeneClean both it and vector.

X116

GeneClean = vector + cDNA insert (#76)

	volume	^{2.5V} NaI	glassmilk
insert -	150 μ l	375 μ l	10 μ l
vector -	150 μ l	375 μ l	10 μ l

Since ligation did not work between vector + cDNA,
need to make sure ends of cDNA are blunt

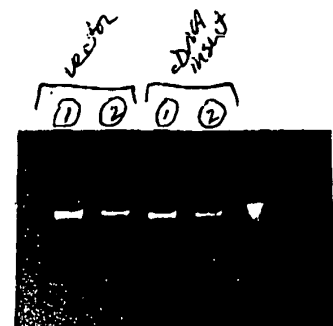
Remove protruding 3' termini from cDNA insert

Combine: 15 μ l of genecleaned mSR-BI cDNA insert
 1 μ l of 1:1:1:1 mix of dNTPs (25mM of each) \Rightarrow final 1.25mM
 2 μ l of NEB Buffer 2 10X (final: 10mM Tris, 10mM MgCl₂, 50mM NaCl,
 1mM DTT pH 7.9)
 2.0 μ l ^{add H₂O} T4 DNA Polymerase (3 U/ μ l)
 Incubate 15 min 12°C

Inactivate polymerase by heating to 75°C for 10 min (11-11:10 am)

Run vector + cDNA insert on minigel to quantitate amts

1 μ l + 2 μ l TE $\xrightarrow{1 \mu l}$ + 2 μ l TE
 ① $\xrightarrow{1 \mu l}$ ②
 run 3 μ l + 2 μ l 2x blue juice = 0.67
 run 3 μ l + 2 μ l 2x blue juice = 0.22



For a 1 vector : 2 insert molar ratio
 use equal μ g of vector + insert
 Looks like vector stock = 1.5x cDNA

ligate cDNA into vector

Ligate cDNA into vector					
Ligation	blunt pcDNA1 CIPed	MSR-B1 blunt cDNA	H ₂ O	BRL 5 X 74 DNA Lig. buffer	BRL T4 DNA Ligase (1U/μl)
1	3μl	-	4.5μl	2μl	0.5μl
2	3μl	4.5μl	-	2μl	0.5μl
3	1μl uncIPed vector -	-	6.5μl	2μl	0.5μl

Mix well, spin & incubate 12-16°C ($\sim 15^\circ\text{C}$) 12:15 pm - 10:30 PM
($\sim 48\text{ hrs}$)

Transform MC1061/P3

transf	amt	results # colonies
1 Lig #1	5 μ l	123
2 Lig #2	5 μ l	32
3 Lig #3	5 μ l	33
4 TE only	5 μ l	
5 pCDNA1-300ng/ μ l 5 μ l	4 μ l	>1000

transformation worked ~~but~~
~~1000 colonies~~ but
 other results
 don't make
 sense

- 1) Add 5 μ l of above DNA to thawed component MC1061/R3.
Mix by gentle shaking
Store on ice 30' (10:40-11:10)
- 2) Transfer to circulating water bath at 42°C.
Incubate exactly 90 sec.
- 3) Rapidly transfer to ice bath. Allow cells to chill 1-2 min.
Add 400 μ l LB warm to 37°C & transfer to shaking incubator at 37°C.
- 4) Plate onto LB Amp^r (15 μ g/ml / 8 μ g/ml)
100 μ l / 100 mm dish Incubate 37°C O.N.

Ran ligation rxns on gel to check



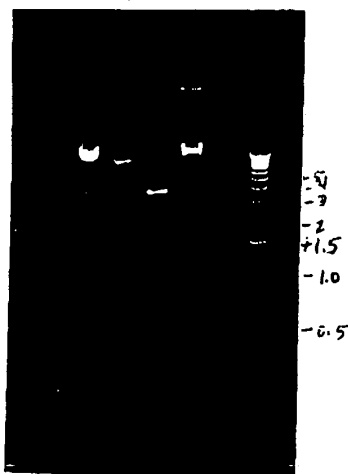
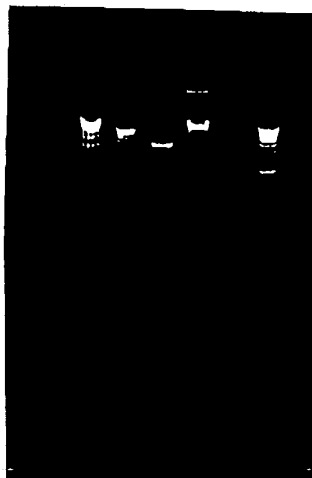
Lig

- #1 - one piece but 6 Kb! ^{see below} should be 4 Kb. Must have cut the wrong vector! Redo preparation of blunt-cut cIPed pcDNA1
- #2 - some ligations appear to have worked possibly cDNA-cDNA worked best. Next time cut way back on amt of cDNA: vector.
- #3 - can't see any DNA

Run with 1 Kb standards

Results:

blunt cut pcDNA1 is 4 Kb as it should be
XHindIII stds are junk



X167

Redo Ligations

<u>Ligation</u>	blunt pcDNA1 CIPed	MSR-BI blunt cDNA	✓ H ₂ O	✓ BRL 5X T4 DNA Lig buffer	BRL T4 DNA Ligase (14 µl)
1	1 µl	-	14	4 µl	1 µl
2	1 µl	1 µl	13	4	1
3	1 µl	1 µl of 1:5	13	4	1
4	1 µl of 1:5	1 µl of 1:5	13	4	1
5	1 µl of 1:5	-	14	4	1

Mix well, spin & incubate 17-16°C (submerged) O.N. (5pm - 2pm)

Transform

			Results # colonies
1	Lig #1 - 5 µl	780 µl comp MC1061/TS CRO	68
2	2 - 5 µl		136
3	3 - 5 µl		136
4	4 - 5 µl		65
5	5 - 5 µl		19 + ~30 in one large group
6	TE - 5 µl		5
7	pcDNA1 - 1 µl		72000

On ice 30' 2:30 3pm
Shake 42°C 90 sec

On ice 1-2 min

Add 40 µl LB & shake

Plate onto LB A/T (37°C 45') (#1-4 my plates, #5-7 X-ray's plates)
100 µl

PCR colonies

Purpose: Determine if colonies from transformation plate #2 contain mR-BI in correct orientation.

Set A (determine if insert within): T7 + ST6 primers

Set B (determine orientation): T7 + 05A4.4B

For 55 rxns of 70 μ l each

110 μ l 10x PCR buffer (GG)
 275 μ l T7 primer (20 μ mol/l) (VA)
 725.7 μ l H₂O
 2.2 μ l dATP
 2.2 μ l dCTP
 2.2 μ l dGTP
 2.2 μ l dTTP
 5.5 μ l Tag polymerase

(A)	412.5 μ l	412.5 μ l (B)
	+ 137.5 μ l ST6 (20 μ mol/l)	+ 2 μ l stock 05A4.4B (unknown conc.) + 135.5 μ l H ₂ O

Pick 20 colonies

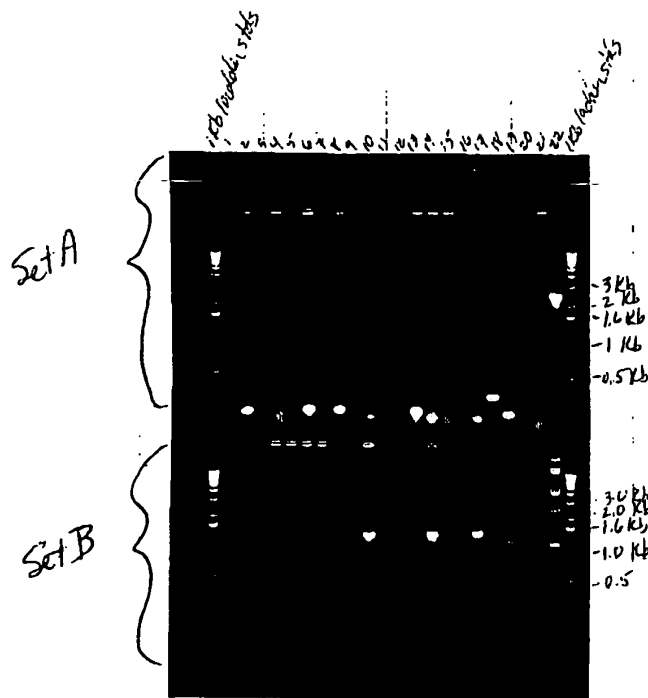
#21 neg control colony from transformation plate #1
 #22 control #26 pure plasmid in SR BI in pCDNA1 backward

From 20 random colonies

10 will probably be vector only (no insert): background...
 10 will " contain DNA
 of which 5 will be backwards
 and 5 will be correct orientation

Run gel on PCR products

Run 1% GTC-Agarose. 1X TAE



Results: Only the positive control pure plasmid #76 (PCR product) worked with the T7 + SP6 primers. However, a band of ~1.3 Kb was present in #10, #14 & #17. The expected size is 1.35 Kb for mSR B1 in correct orientation. Hopefully these are real.

Plasmid midiprep

preps:

2, # 10, # 14, # 17 colonies from ligation/transform plate 2.

Day 1

1. Pick a single colony into 25 mls LB Amp/Tet and grow overnight shaking 37°C.

Day 2

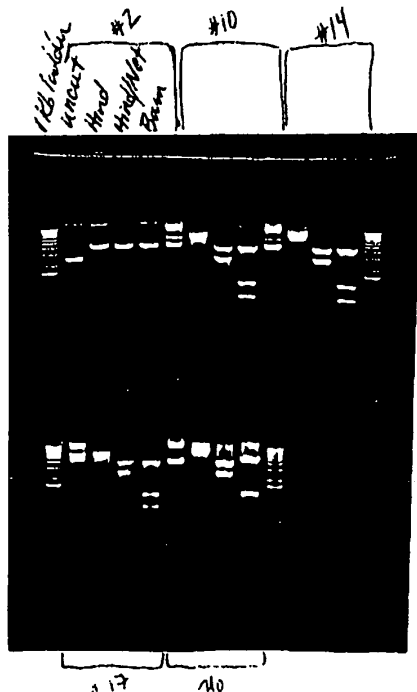
2. Take 400 µl, put into freezer vial, add 100 µl glycerol and freeze at -150C.
3. Transfer half to Falcon 2059 15 ml tube on ice.
4. Spin in SS-34, 9000 rpm, 2 min 4C. Discard supe, add remaining bacteria and respin.
5. Dry pellet as much as possible.
6. Resuspend pellet in 500 µl ice cold solution I by vigorous vortexing.
7. Add 1 ml fresh solution II (0.2 N NaOH, 1% SDS)
for 100 ml: 1 ml 2 N NaOH
0.5 ml 20% SDS
8.5 mls ddH2O
Swirl gently until clear. Do not vortex. Leave on ice 10 min.
8. Add 750 µl solution III (ice-cold). Close tube and mix contents by shaking vigorously several times. Store on ice 5'. A flocculent white precipitate should form.
9. Centrifuge 15', 4°C, 9000 rpm.
10. Recover supe and add equal volume of phenol:chloroform. Mix by vortexing.
11. Spin 9000 rpm, 5'. Recover aq. phase.
12. Add 2 volumes, ethanol r.t., vortex, let stand 5'.
Spin in SS-34 rotor for 15' 9,000 rpm.
13. Carefully aspirate off all liquid (want it dry) and rinse once in cold 70% EtOH. Aspirate again getting any extraneous drops. Airdry 10' minutes.
14. Redissolve in 100 µl TE plus DNase-free RNase (20 µg/ml). Vortex briefly. Incubate 37C/0.5 - 2 hr.
Transfer to sterile eppendorf.
15. Quantitate by dilutions onto EtBr plate.

Digests

Digest	DNA	10X	10X	10X	10X
1	colony 10	2ul	2ul	2ul	2ul
2					
3					
4					
5	colony 10				
6					
7					
8					
9					
10	colony 14				
11					
12					
13	colony 17				
14					
15					
16					
17	#76 msp.B1 (backwards)				
18					
19					
20					

12:45 - 3:45

Run on 1% Seakem GTG TAE gel



Results: Neg control #2 looks like pcDNA1 only. #10 #14 #17 all look same with insert. size ~ 2.5 Kb. Not identical to #76 msp.B1 (backwards). Everything looks good! I think all three #10 #14 #17 are all in correct direction. see next page

X168

DEAE dextran transfections of COS M6 cells**materials:**

- | | |
|---|--|
| 1. 35 mm dishes | 5. CMF PBS |
| 2. DMEM with 10% FBS | 6. DEAE-dextran (10 mg/ml in CMF PBS (autoclaved)) |
| 3. Chloroquine (40 mM in CMF PBS, sterile filtered) | 7. DMSO |
| 4. DNA | 8. cPBS |
| | 9. sterile tips |

method:**day 0 (set up cells)**

Set COS M6 cells in 100 mm dishes

(Set 1 confluent T75 into 2.25 100 mm dishes; or 1.5×10^6 cells/dish in 10 ml DMEM with 10% FBS)**day 1 (transfect)**

1. In sterile polypropylene tubes prepare for each dish add (in order):
 - a) add CMF PBS to 1.9 ml
 - b) DNA - 5 μ g/dish
 - c) 100 μ l of 10 mg/ml DEAE-dextran, vortex well (7 seconds)

tube	# plates	DNA	CMF PBS	DEAE-dextran
1	1	100 DNA (1.27 μ g/ μ l)	1.9 ml	100 μ l
2	3	pmSP-BL (1.27 μ g/ μ l)	30 μ l	300 μ l
3				
4				

2. Rinse cells with 10 mls CMF PBS (37C). Aspirate PBS.
3. Add transfection cocktail from step 1 and distribute evenly. Incubate 30 minutes, distributing liquid every 10 min. 1:30 - 2:00
4. Add 8 ml DMEM 10% FBS + 80 μ M chloroquine and incubate 37C 2.5 hrs. 4:30
5. Aspirate off medium and replace with 5 ml 10% DMSO in DMEM 10% FBS for 2.5 min.
6. Aspirate off and wash once with 10 mls cPBS.
7. Refeed with 10 ml warm DMEM 10% FBS/dish. Incubate overnight.

Lipoprotein 4°C Binding Assay**materials:**

1. 6-well dishes
2. DMEM with 10% FBS
3. iodinated and unlabeled lipoprotein
4. Tris-HCl wash buffer
5. Tris-HCl BSA wash buffer
6. 0.1 N NaOH
7. 10 x 75 tubes

method:**day 0: Set up cells**

Set transfected COS in 6-well dishes at 1×10^6 cells/well in 3 ml/well DMEM + 10% FBS + 1 mM Nubutyrate.

day 1: Binding assay

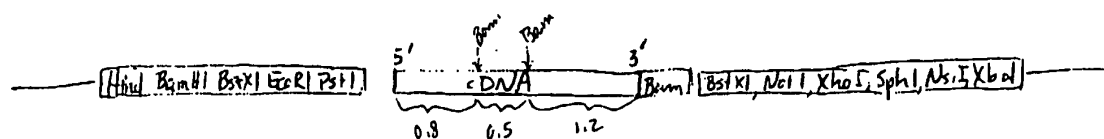
1. Cool cells down on ice for 30 minutes.
2. Refeed cells labeled ligand 1 ml/well (Hams + HEPES + 5% NCLPDS + 10% FBS).
 2 Hot - ^{125}I -lipoprotein: 10 ng/ml ^{125}I -AcLDL #62 (0.55 $\mu\text{Ci}/\mu\text{g}$)
 + Hot + cold: compete titers (at 400 ng/ml)
 Incubate 2 hrs 4°C (in cold room) on shaker.
3. Wash cells (1 ml each)
 3X fast with BSA wash buffer
 2X 5 min with BSA wash buffer
 2X fast with Tris wash buffer
4. Add 1.0 ml 0.1 N NaOH. Leave 20 min r.t. on shaker
5. Remove 50 μl to 10 x 75 tube and freeze for Lowry.
6. Count 500 μl of rest of sample.
7. Count 10 μl of medium + label for specific activity.

AcLDL #55 4.6 ng/ml
 LDL #16/B 39
 HDL #3 31.2
 VLDL #5 26.7

309 μl ^{125}I -AcLDL #62 + 17 ml Hams + 5% NCLPDS + 10 mM HEPES

4 ml + 348 μl AcLDL #55
 7 ml + 70.5 μl LDL #16/B
 7 ml + 75.6 μl HDL #3
 7 ml + 38.6 μl VLDL #5

msr-BI in correct orientation:



msr-BI (#76) in incorrect orientation:

